

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/403,075

DATE: 09/14/2000  
 TIME: 17:14:11

Input Set : A:\Pto.amc  
 Output Set: N:\CRF3\09142000\I403075.raw

2 <110> APPLICANT: Johnson, Gary L.  
 4 <120> TITLE OF INVENTION: MEKK1 PROTEINS AND FRAGMENTS THEREOF FOR USE IN REGULATING  
 5 APOPTOSIS  
 W--> 6 <130> FILE REFERENCE: CPI-042CPFC  
 C--> 8 <140> CURRENT APPLICATION NUMBER: US/09/403,075  
 C--> 9 <141> CURRENT FILING DATE: 2000-05-10  
 11 <160> NUMBER OF SEQ ID NOS: 21  
 13 <170> SOFTWARE: PatentIn Ver. 2.0  
 15 <210> SEQ ID NO: 1  
 16 <211> LENGTH: 3260  
 17 <212> TYPE: DNA  
 18 <213> ORGANISM: Mus musculus  
 20 <221> NAME/KEY: CDS  
 21 <222> LOCATION: (486)..(2501)  
 23 <400> SEQUENCE: 1  
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 28 ctacagtgtt ggaactctgc aagggccaag caggagagct ggcgggttgg agagaaatac 180  
 30 ttaaagctgg gtccatcggg gttggtgggt tgcattacgt ctttaagttgt atccttggaa 240  
 32 accaagctga atcaaaacaac tggcaagaac tgctgggtcg cctctgtctt atagacaggt 300  
 34 tgctgttggg atttctctgt gaattctatc ctcatattgt cagtactgat gtctcacaag 360  
 36 ctgagcctgt tgaaatcagg tacaagaagc tgctctccct ctttaaccttt gccttgcaat 420  
 38 ccattgacaa ttcccaactcg atggttgcca agctctctcg gaggatataat ctgagctctg 480  
 40 ccagg atg gtg acc gca gtg ccc gct gtg ttt tcc aag ctg gta acc atg 530  
 41 Met Val Thr Ala Val Pro Ala Val Phe Ser Lys Leu Val Thr Met  
 42 1 5 10 15  
 44 ctt aat gct tct ggc tcc acc cac ttc acc agg atg cgc cgg cgt ctg 578  
 45 Leu Asn Ala Ser Gly Ser Thr His Phe Thr Arg Met Arg Arg Arg Leu  
 46 20 25 30  
 48 atg gct atc gcg gat gag gta gaa att gcc gag gtc atc cag ctg ggt 626  
 49 Met Ala Ile Ala Asp Glu Val Glu Ile Ala Glu Val Ile Gln Leu Gly  
 50 35 40 45  
 52 gtg gag gac act gtg gat ggg cat cag gac agc tta cag gcc gtg gcc 674  
 53 Val Glu Asp Thr Val Asp Gly His Gln Asp Ser Leu Gln Ala Val Ala  
 54 50 55 60  
 56 ccc acc agc tgt cta gaa aac agc tcc ctt gag cac aca gtc cat aga 722  
 57 Pro Thr Ser Cys Leu Glu Asn Ser Ser Leu Glu His Thr Val His Arg  
 58 65 70 75  
 60 gag aaa act gga aaa gga cta agt gct acg aga ctg agt gcc agc tcg 770  
 61 Glu Lys Thr Gly Lys Gly Leu Ser Ala Thr Arg Leu Ser Ala Ser Ser  
 62 80 85 90 95  
 64 gag gac att tct gac aga ctg gcc ggc gtc tct gta gga ctt ccc agc 818  
 65 Glu Asp Ile Ser Asp Arg Leu Ala Gly Val Ser Val Gly Leu Pro Ser  
 66 100 105 110  
 68 tca aca aca aca gaa caa cca aag cca gcg gtt caa aca aaa ggc aga 866  
 69 Ser Thr Thr Thr Glu Gln Pro Lys Pro Ala Val Gln Thr Lys Gly Arg  
 70 115 120 125

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72 ccc cac agt cag tgt ttg aac tcc tcc cct ttg tct cat gct caa tta 914
73 Pro His Ser Gln Cys Leu Asn Ser Ser Pro Leu Ser His Ala Gln Leu
74      130      135      140
76 atg ttc cca gca cca tca gcc cct tgt tcc tct gcc ccg tct gtc cca 962
77 Met Phe Pro Ala Pro Ser Ala Pro Cys Ser Ser Ala Pro Ser Val Pro
78      145      150      155
80 gat att tct aag cac aga ccc cag gca ttt gtt ccc tgc aaa ata cct 1010
81 Asp Ile Ser Lys His Arg Pro Gln Ala Phe Val Pro Cys Lys Ile Pro
82 160      165      170      175
84 tcc gca tct cct cag aca cag cgc aag ttc tct cta caa ttc cag agg 1058
85 Ser Ala Ser Pro Gln Thr Gln Arg Lys Phe Ser Leu Gln Phe Gln Arg
86      180      185      190
88 aac tgc tct gaa cac cga gac tca gac cag ctc tcc cca gtc ttc act 1106
89 Asn Cys Ser Glu His Arg Asp Ser Asp Gln Leu Ser Pro Val Phe Thr
90      195      200      205
92 cag tca aga ccc cca ccc tcc agt aac ata cac agg cca aag cca tcc 1154
93 Gln Ser Arg Pro Pro Pro Ser Ser Asn Ile His Arg Pro Lys Pro Ser
94      210      215      220
96 cga ccc gtt ccg ggc agt aca agc aaa cta ggg gac gcc aca aaa agt 1202
97 Arg Pro Val Pro Gly Ser Thr Ser Lys Leu Gly Asp Ala Thr Lys Ser
98      225      230      235
100 agc atg aca ctt gat ctg ggc agt gct tcc agg tgt gac gac agc ttt 1250
101 Ser Met Thr Leu Asp Leu Gly Ser Ala Ser Arg Cys Asp Asp Ser Phe
102 240      245      250      255
104 ggc ggc ggc ggc aac agt ggc aac gcc gtc ata ccc agc gac gag aca 1298
105 Gly Gly Gly Gly Asn Ser Gly Asn Ala Val Ile Pro Ser Asp Glu Thr
106      260      265      270
108 gtg ttc acg ccg gtg gag gac aag tgc agg tta gat gtg aac acc gag 1346
109 Val Phe Thr Pro Val Glu Asp Lys Cys Arg Leu Asp Val Asn Thr Glu
110      275      280      285
112 ctc aac tcc agc atc gag gac ctt ctt gaa gca tcc atg cct tca agt 1394
113 Leu Asn Ser Ser Ile Glu Asp Leu Leu Glu Ala Ser Met Pro Ser Ser
114      290      295      300
116 gac acg aca gtc act ttc aag tcc gaa gtc gcc gtc ctc tct ccg gaa 1442
117 Asp Thr Thr Val Thr Phe Lys Ser Glu Val Ala Val Leu Ser Pro Glu
118      305      310      315
120 aag gcc gaa aat gac gac acc tac aaa gac gac gtc aat cat aat caa 1490
121 Lys Ala Glu Asn Asp Asp Thr Tyr Lys Asp Asp Val Asn His Asn Gln
122 320      325      330      335
124 aag tgc aaa gaa aag atg gaa gct gaa gag gag gct tta gcg atc 1538
125 Lys Cys Lys Glu Lys Met Glu Ala Glu Glu Glu Glu Ala Leu Ala Ile
126      340      345      350
128 gcc atg gcg atg tca gcg tct cag gat gcc ctc ccc atc gtc cct cag 1586
129 Ala Met Ala Met Ser Ala Ser Gln Asp Ala Leu Pro Ile Val Pro Gln
130      355      360      365
132 ctg cag gtg gaa aat gga gaa gat att atc atc att cag cag gac aca 1634
133 Leu Gln Val Glu Asn Gly Glu Asp Ile Ile Ile Ile Gln Gln Asp Thr
134      370      375      380
136 cca gaa act ctt cca gga cat acc aaa gcg aaa cag cct tac aga gaa 1682

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137 Pro Glu Thr Leu Pro Gly His Thr Lys Ala Lys Gln Pro Tyr Arg Glu
138      385      390      395
140 gac gct gag tgg ctg aaa ggc cag cag ata ggc ctc gga gca ttt tct 1730
141 Asp Ala Glu Trp Leu Lys Gly Gln Gln Ile Gly Leu Gly Ala Phe Ser
142 400      405      410      415
144 tcc tgt tac caa gca cag gat gtg ggg act ggg act tta atg gct gtg 1778
145 Ser Cys Tyr Gln Ala Gln Asp Val Gly Thr Gly Thr Leu Met Ala Val
146      420      425      430
148 aaa cag gtg acg tac gtc aga aac aca tcc tcc gag cag gag gag gtg 1826
149 Lys Gln Val Thr Tyr Val Arg Asn Thr Ser Ser Glu Gln Glu Glu Val
150      435      440      445
152 gtg gaa gcg ttg agg gaa gag atc cgg atg atg ggt cac ctc aac cat 1874
153 Val Glu Ala Leu Arg Glu Glu Ile Arg Met Met Gly His Leu Asn His
154      450      455      460
156 cca aac atc atc cgg atg ctg ggg gcc acg tgc gag aag agc aac tac 1922
157 Pro Asn Ile Ile Arg Met Leu Gly Ala Thr Cys Glu Lys Ser Asn Tyr
158      465      470      475
160 aac ctc ttc att gag tgg atg gcg gga gga tct gtg gct cac ctc ttg 1970
161 Asn Leu Phe Ile Glu Trp Met Ala Gly Gly Ser Val Ala His Leu Leu
162 480      485      490      495
164 agt aaa tac gga gct ttc aag gag tca gtc gtc att aac tac act gag 2018
165 Ser Lys Tyr Gly Ala Phe Lys Glu Ser Val Val Ile Asn Tyr Thr Glu
166      500      505      510
168 cag tta ctg cgt ggc ctt tcc tat ctc cac gag aac cag atc att cac 2066
169 Gln Leu Leu Arg Gly Leu Ser Tyr Leu His Glu Asn Gln Ile Ile His
170      515      520      525
172 aga gac gtc aaa ggt gcc aac ctg ctc att gac agc acc ggt cag agg 2114
173 Arg Asp Val Lys Gly Ala Asn Leu Leu Ile Asp Ser Thr Gly Gln Arg
174      530      535      540
176 ctg aga att gca gac ttt gga gct gct gcc agg ttg gca tca aaa gga 2162
177 Leu Arg Ile Ala Asp Phe Gly Ala Ala Ala Arg Leu Ala Ser Lys Gly
178      545      550      555
180 acc ggt gca gga gag ttc cag gga cag tta ctg ggg aca att gca ttc 2210
181 Thr Gly Ala Gly Glu Phe Gln Gly Gln Leu Leu Gly Thr Ile Ala Phe
182 560      565      570      575
184 atg gcg cct gag gtc cta aga ggt cag cag tat ggt agg agc tgt gat 2258
185 Met Ala Pro Glu Val Leu Arg Gly Gln Gln Tyr Gly Arg Ser Cys Asp
186      580      585      590
188 gta tgg agt gtt ggc tgc gcc att ata gaa atg gct tgt gca aaa cca 2306
189 Val Trp Ser Val Gly Cys Ala Ile Ile Glu Met Ala Cys Ala Lys Pro
190      595      600      605
192 cct tgg aat gca gaa aaa cac tcc aat cat ctc gcc ttg ata ttt aag 2354
193 Pro Trp Asn Ala Glu Lys His Ser Asn His Leu Ala Leu Ile Phe Lys
194      610      615      620
196 att gct agc gca act act gca ccg tcc atc ccg tca cac ctg tcc ccg 2402
197 Ile Ala Ser Ala Thr Thr Ala Pro Ser Ile Pro Ser His Leu Ser Pro
198      625      630      635
200 ggt ctg cgc gac gtg gcc gtg cgc tgc tta gaa ctt cag cct cag gac 2450
201 Gly Leu Arg Asp Val Ala Val Arg Cys Leu Glu Leu Gln Pro Gln Asp

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202 640          645          650          655          2498
204 cgg cct ccg tcc aga gag ctg ctg aaa cat ccg gtc ttc cgt acc acg
205 Arg Pro Pro Ser Arg Glu Leu Leu Lys His Pro Val Phe Arg Thr Thr
206          660          665          670
208 tgg tagttaattg ttcagatcag ctctaattgga gacaggatat cgaaccggga 2551
209 Trp
211 gagagaaaaag agaacttgtg ggcgaccatg ccgctaaccg cagccctcac gccactgaac 2611
213 agccagaaaac ggggcccagcg ggggaaccgta cctaagcatg tgattgacaa atcatgacct 2671
215 gtacctaagc tcgatatgca gacatctaca gctcgtgcag gaactgcaca ccgtgccttt 2731
217 cacaggactg gctctggggg accaggaagg cgatggagtt tgcattgacta aagaacagaa 2791
219 gcataaaattt atttttggag cactttttca gctaatacagt attaccatgt acatcaacat 2851
221 gcccgcacaca ttcaaactc agactgtccc agatgtcaag atccactgtg tttgagtttg 2911
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225 taatattctt attttctttg gatcaaaagct ggactgaaaa ttgtactgtg taattatttt 3031
227 tgtgttttta atgtttattg gtactcgaat tgtaaataac gtctactgct gtttattcca 3091
229 gtttctacta cctcaggtgt cctatagatt tttcttctac caaagttcac tctcagaatg 3151
231 aaattctacg tgctgtgtga ctatgactcc taagacttcc agggcttaag ggctaactcc 3211
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237 <211> LENGTH: 672
238 <212> TYPE: PRT
239 <213> ORGANISM: Mus musculus
241 <400> SEQUENCE: 2
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249 35 40 45
251 Glu Asp Thr Val Asp Gly His Gln Asp Ser Leu Gln Ala Val Ala Pro
252 50 55 60
254 Thr Ser Cys Leu Glu Asn Ser Ser Leu Glu His Thr Val His Arg Glu
255 65 70 75 80
257 Lys Thr Gly Lys Gly Leu Ser Ala Thr Arg Leu Ser Ala Ser Ser Glu
258 85 90 95
260 Asp Ile Ser Asp Arg Leu Ala Gly Val Ser Val Gly Leu Pro Ser Ser
261 100 105 110
263 Thr Thr Thr Glu Gln Pro Lys Pro Ala Val Gln Thr Lys Gly Arg Pro
264 115 120 125
266 His Ser Gln Cys Leu Asn Ser Ser Pro Leu Ser His Ala Gln Leu Met
267 130 135 140
269 Phe Pro Ala Pro Ser Ala Pro Cys Ser Ser Ala Pro Ser Val Pro Asp
270 145 150 155 160
272 Ile Ser Lys His Arg Pro Gln Ala Phe Val Pro Cys Lys Ile Pro Ser
273 165 170 175
275 Ala Ser Pro Gln Thr Gln Arg Lys Phe Ser Leu Gln Phe Gln Arg Asn
276 180 185 190
278 Cys Ser Glu His Arg Asp Ser Asp Gln Leu Ser Pro Val Phe Thr Gln
279 195 200 205

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281 Ser Arg Pro Pro Pro Ser Ser Asn Ile His Arg Pro Lys Pro Ser Arg
282      210      215      220
284 Pro Val Pro Gly Ser Thr Ser Lys Leu Gly Asp Ala Thr Lys Ser Ser
285 225      230      235      240
287 Met Thr Leu Asp Leu Gly Ser Ala Ser Arg Cys Asp Asp Ser Phe Gly
288      245      250      255
290 Gly Gly Gly Asn Ser Gly Asn Ala Val Ile Pro Ser Asp Glu Thr Val
291      260      265      270
293 Phe Thr Pro Val Glu Asp Lys Cys Arg Leu Asp Val Asn Thr Glu Leu
294      275      280      285
296 Asn Ser Ser Ile Glu Asp Leu Leu Glu Ala Ser Met Pro Ser Ser Asp
297      290      295      300
299 Thr Thr Val Thr Phe Lys Ser Glu Val Ala Val Leu Ser Pro Glu Lys
300 305      310      315      320
302 Ala Glu Asn Asp Asp Thr Tyr Lys Asp Asp Val Asn His Asn Gln Lys
303      325      330      335
305 Cys Lys Glu Lys Met Glu Ala Glu Glu Glu Ala Leu Ala Ile Ala
306      340      345      350
308 Met Ala Met Ser Ala Ser Gln Asp Ala Leu Pro Ile Val Pro Gln Leu
309      355      360      365
311 Gln Val Glu Asn Gly Glu Asp Ile Ile Ile Ile Gln Gln Asp Thr Pro
312      370      375      380
314 Glu Thr Leu Pro Gly His Thr Lys Ala Lys Gln Pro Tyr Arg Glu Asp
315 385      390      395      400
317 Ala Glu Trp Leu Lys Gly Gln Gln Ile Gly Leu Gly Ala Phe Ser Ser
318      405      410      415
320 Cys Tyr Gln Ala Gln Asp Val Gly Thr Gly Thr Leu Met Ala Val Lys
321      420      425      430
323 Gln Val Thr Tyr Val Arg Asn Thr Ser Ser Glu Gln Glu Val Val
324      435      440      445
326 Glu Ala Leu Arg Glu Glu Ile Arg Met Met Gly His Leu Asn His Pro
327      450      455      460
329 Asn Ile Ile Arg Met Leu Gly Ala Thr Cys Glu Lys Ser Asn Tyr Asn
330 465      470      475      480
332 Leu Phe Ile Glu Trp Met Ala Gly Gly Ser Val Ala His Leu Leu Ser
333      485      490      495
335 Lys Tyr Gly Ala Phe Lys Glu Ser Val Val Ile Asn Tyr Thr Glu Gln
336      500      505      510
338 Leu Leu Arg Gly Leu Ser Tyr Leu His Glu Asn Gln Ile Ile His Arg
339      515      520      525
341 Asp Val Lys Gly Ala Asn Leu Leu Ile Asp Ser Thr Gly Gln Arg Leu
342      530      535      540
344 Arg Ile Ala Asp Phe Gly Ala Ala Ala Arg Leu Ala Ser Lys Gly Thr
345 545      550      555      560
347 Gly Ala Gly Glu Phe Gln Gly Gln Leu Leu Gly Thr Ile Ala Phe Met
348      565      570      575
350 Ala Pro Glu Val Leu Arg Gly Gln Gln Tyr Gly Arg Ser Cys Asp Val
351      580      585      590
353 Trp Ser Val Gly Cys Ala Ile Ile Glu Met Ala Cys Ala Lys Pro Pro

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VERIFICATION SUMMARY

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Input Set : A:\Pto.amc

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L:8 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date